STIC Database Tracking Number: 163616

TO: Nita M Minnifield Location: rem/3c01/3c18 Art Unit: 1645 Wednesday, May 18, 2005 Case Serial Number: 09/942098	**From: Mary Jane Ruhl** Location: Biotech-Chem Library Remsen 1-A-62 Phone: 571-272-2524 maryjane.ruhl@uspto.gov

Search Notes

Examiner Minnifield,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

Reviewed
5/3?/05
MM

From: Chan, Christina
Sent: Tuesday, May 17, 2005 8:55 AM
To: Minnifield, Nita; STIC-Biotech/ChemLib
Subject: RE: interference sequence search

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----
From: Minnifield, Nita
Sent: Monday, May 16, 2005 6:51 PM
To: Chan, Christina
Subject: interference sequence search

Christina,
Please approve, 2 month amdt. due.

STIC 09/942098

Please do a commercial and interference sequence search on SEQ ID NO: 30 of this application.

Please do an interference sequence search on SEQ ID NO: 1 and 2, and aa 187-203 of SEQ ID NO: 2.

Please provide a paper copy of all results.

Thanks,
Minnifield,
71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: May 17, 2005, 15:24:21 ; Search time 175 Seconds
(without alignments)
49.745 Million cell updates/sec

Title: US-09-942-098-30
Perfect score: 83
Sequence: 1 SNKTRIDEANQRATKML 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID		Description
1	83	100.0	124	2	O93578	O93578	brachydanio
2	83	100.0	143	2	Q9GM34	Q9GM34	macaca fasc
3	83	100.0	198	2	Q6PC84	Q6PC84	brachydanio
4	83	100.0	203	1	SN2B_CARAU	P36978	carassius a
5	83	100.0	203	2	O93579	O93579	brachydanio
6	83	100.0	203	2	Q6PC54	Q6PC54	brachydanio
7	83	100.0	204	1	SN2A_CARAU	P36977	carassius a
8	83	100.0	204	2	Q70SJ6	Q70SJ6	lateolabrax
9	83	100.0	206	1	SN25_CHICK	P60878	gallus gall
10	83	100.0	206	1	SN25_HUMAN	P60880	homo sapien
11	83	100.0	206	1	SN25_MACMU	P60877	macaca mula
12	83	100.0	206	1	SN25_MOUSE	P60879	mus musculu
13	83	100.0	206	1	SN25_RAT	P60881	rattus norv
14	79	95.2	204	2	Q6P3I7	Q6P3I7	brachydanio
15	69	83.1	206	2	Q8AXM1	Q8AXM1	xenopus lae
16	69	83.1	206	2	Q8AXM2	Q8AXM2	xenopus lae
17	69	83.1	206	2	Q640W4	Q640W4	xenopus lae
18	66	79.5	214	2	Q72ZV4	Q72ZV4	xenopus lae
19	65	78.3	210	1	SN25_TORMA	P36976	torpedo mar
20	65	78.3	212	2	Q8T3S4	Q8T3S4	loligo peal
21	61	73.5	137	2	Q661D7	Q661D7	brachydanio
22	60	72.3	204	2	Q8JIS7	Q8JIS7	xenopus lae
23	53	63.9	212	2	O01389	O01389	hirudo medi
24	50	60.2	210	1	SN23_MOUSE	Q9044	mus musculu
25	50	60.2	210	1	SN23_RAT	O70377	rattus norv
26	50	60.2	221	2	Q9D3L3	Q9D3L3	mus musculu
27	47	56.6	220	2	Q869G6	Q869G6	lymnaea sta
28	46	55.4	211	1	SN23_HUMAN	O00161	homo sapien
29	46	55.4	2315	2	Q95ZK3	Q95ZK3	caenorhabdi
30	46	55.4	2350	2	Q7JNN3	Q7JNN3	caenorhabdi
31	46	55.4	2396	2	Q23081	Q23081	caenorhabdi
32	45	54.2	83	2	O85431	O85431	pseudomonas
33	45	54.2	83	2	O85439	O85439	pseudomonas
34	45	54.2	83	2	O85440	O85440	pseudomonas
35	45	54.2	125	2	O96576	O96576	leucophaea
36	45	54.2	212	1	SN25_DROME	P36975	drosophila
37	44.5	53.6	191	2	Q8ZY72	Q8ZY72	pyrobaculum
38	44	53.0	90	2	O96578	O96578	leucophaea
39	44	53.0	207	2	O62414	O62414	caenorhabdi
40	44	53.0	213	2	Q7PUS1	Q7PUS1	anopheles g
41	44	53.0	649	2	Q7NAR4	Q7NAR4	mycoplasma
42	44	53.0	776	1	Q89QI8	Q89QI8	bradyrhizob
43	44	53.0	2090	1	NIN_HUMAN	Q8N4C6	homo sapien
44	43.5	52.4	55	2	Q8NCR8	Q8NCR8	homo sapien
45	43	51.8	353	2	Q8FNU8	Q8FNU8	corynebacte

ALIGNMENTS

RESULT 1
O93578

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ID   O93578      PRELIMINARY;      PRT;    124 AA.
AC   O93578;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Synaptosome-associated protein 25.1 (Fragment).
GN   Name=snap25a; Synonyms=Snap;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9057281; PubMed=9843147;
RX   DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNR1>3.3.CO;2-Z;
RA   Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
RA   Larhammar D.;
RT   "Cloning of two loci for synapse protein Snap25 in zebrafish:
RT   comparison of paralogous linkage groups suggests loss of one locus in
RT   the mammalian lineage.";
RL   J. Neurosci. Res. 54:563-573 (1998).
CC   -!- SIMILARITY: Belongs to the SNAP-25 family.
DR   EMBL; AF091593; AAC64289.1; -.
DR   HSSP; Q8T3S4; 1L4A.
DR   ZFIN; ZDB-GENE-980526-468; snap25a.
DR   GO; GO:0019717; C:synaptosome; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR002197; HTH_Fis.
DR   InterPro; IPR000928; SNAP-25.
DR   InterPro; IPR010989; t-snare.
DR   InterPro; IPR000727; T_SNARE.
DR   Pfam; PF00835; SNAP-25; 1.
DR   Pfam; PF05739; SNARE; 1.
DR   PRINTS; PR01590; HTHFIS.
DR   SMART; SM00397; t_SNARE; 1.
DR   PROSITE; PS50192; T_SNARE; 1.
KW   Synaptosome.
FT   NON_TER       1      1
SQ   SEQUENCE   124 AA;  13616 MW;  50B27DBDB33D958C CRC64;
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Query Match 100.0%; Score 83; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 SNKTRIDEANQRATKML  17
         |||||||||||||||||
Db  105 SNKTRIDEANQRATKML 121
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RESULT 2

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            GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:    May 17, 2005, 15:25:17 ; Search time 38 Seconds
                                     (without alignments)
                                     43.044 Million cell updates/sec

Title:          US-09-942-098-30
Perfect score:  83
Sequence:       1 SNKTRIDEANQRATKML 17
Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:       283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  PIR_79:*
            1: Pir1:*
            2: Pir2:*
            3: Pir3:*
            4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	203	2	I50481	synapse protein SN
2	83	100.0	204	2	I50480	synapse protein SN
3	83	100.0	206	2	A37861	synaptosomal-assoc
4	83	100.0	206	2	I53735	nerve terminal pro
5	83	100.0	206	2	I67823	nerve terminal pro
6	83	100.0	206	2	A33623	synaptosomal-assoc
7	65	78.3	210	2	I50552	synapse protein -
8	50	60.2	210	2	JC5512	SNARE protein 23 -
9	46	55.4	158	2	JC5297	vesicle-membrane f
10	46	55.4	211	2	JC5296	vesicle-membrane f
11	46	55.4	2288	2	T29999	hypothetical prote
12	44	53.0	234	2	T26553	hypothetical prote
13	42	50.6	83	2	A33854	outer membrane lip
14	42	50.6	401	2	E81436	transmembrane-tran
15	42	50.6	420	2	S50562	hypothetical prote
16	41	49.4	393	2	T32127	hypothetical prote
17	41	49.4	494	2	S64386	pre-mRNA splicing
18	41	49.4	642	2	G90551	lipoprotein [impor
19	40	48.2	540	2	T34187	hypothetical prote
20	40	48.2	575	2	F96966	methyl-accepting c
21	39.5	47.6	1314	2	T09481	mating type silenc
22	39	47.0	243	2	T20653	hypothetical prote
23	39	47.0	680	2	H70347	outer membrane pro
24	38.5	46.4	918	2	G88545	protein F59B2.12 [
25	38.5	46.4	943	2	S31132	hypothetical prote
26	38	45.8	142	2	T48816	hypothetical prote
27	38	45.8	151	2	G95369	SyrB2 transcriptio
28	38	45.8	176	2	D72668	hypothetical prote
29	38	45.8	181	2	A45422	ADP-ribosylation f
30	38	45.8	181	2	JC4946	ADP-ribosylation f
31	38	45.8	217	2	A47483	cysteine-rich omeg
32	38	45.8	219	2	AB1996	hypothetical prote
33	38	45.8	294	2	S68784	cathepsin L - Para
34	38	45.8	317	2	A72295	conserved hypothet
35	38	45.8	414	2	T26205	hypothetical prote
36	38	45.8	465	2	T16618	hypothetical prote
37	38	45.8	586	1	C64988	probable sulfatase
38	38	45.8	586	2	H91013	probable sulfatase
39	38	45.8	586	2	B85858	probable sulfatase
40	38	45.8	643	2	T32269	hypothetical prote
41	38	45.8	869	2	H89864	hypothetical prote
42	38	45.8	1272	2	C96637	hypothetical prote
43	38	45.8	1578	2	S76238	hypothetical prote
44	37	44.6	150	2	T19447	hypothetical prote
45	37	44.6	227	2	D83271	probable ATP-bindi

ALIGNMENTS

```
RESULT 1
I50481
synapse protein SNAP-25 - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50481
R;Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Accession: I50481
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-203 <RIS>
A;Cross-references: UNIPROT:P36978; GB:L22976; NID:g349430; PIDN:AAA16538.1; PID:g34943
C;Genetics:
A;Gene: SNAP-25

Query Match             100.0%;  Score 83;  DB 2;  Length 203;
Best Local Similarity   100.0%;  Pred. No. 8.6e-07;
Matches  17;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 SNKTRIDEANQRATKML 17
           |||||||||||||||||
Db   184 SNKTRIDEANQRATKML 200


RESULT 2
I50480
synapse protein SNAP-25 - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50480
R;Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Accession: I50480
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-204 <RIS>
A;Cross-references: UNIPROT:P36977; GB:L22973; NID:g349426; PIDN:AAA16537.1; PID:g34942
C;Genetics:
A;Gene: SNAP-25

Query Match             100.0%;  Score 83;  DB 2;  Length 204;
Best Local Similarity   100.0%;  Pred. No. 8.7e-07;
Matches  17;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 SNKTRIDEANQRATKML 17
           |||||||||||||||||
Db   185 SNKTRIDEANQRATKML 201
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                    GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:      May 17, 2005, 15:26:17 ; Search time 44 Seconds
                                       (without alignments)
                                       28.842 Million cell updates/sec

Title:           US-09-942-098-30
Perfect score:   83
Sequence:        1 SNKTRIDEANQRATKML 17

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters:          513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Issued Patents AA:*
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           2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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           4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
           5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
           6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	83	100.0	17	2	US-08-743-894B-1	Sequence 1, Appli
2	83	100.0	17	2	US-08-743-894B-37	Sequence 37, Appl
3	83	100.0	20	3	US-08-819-286-9	Sequence 9, Appli
4	83	100.0	26	3	US-08-819-286-8	Sequence 8, Appli
5	83	100.0	37	3	US-08-819-286-4	Sequence 4, Appli
6	83	100.0	70	2	US-08-760-001-10	Sequence 10, Appl
7	83	100.0	70	3	US-09-015-960-10	Sequence 10, Appl
8	83	100.0	70	4	US-09-534-572-10	Sequence 10, Appl
9	83	100.0	116	4	US-09-962-360B-11	Sequence 11, Appl
10	83	100.0	206	1	US-08-393-985-18	Sequence 18, Appl
11	83	100.0	206	4	US-08-819-286-1	Sequence 1, Appli
12	83	100.0	206	4	US-09-949-016-6311	Sequence 6311, A
13	83	100.0	219	4	US-09-949-016-10671	Sequence 10671, A
14	80	96.4	17	2	US-08-743-894B-18	Sequence 18, Appl
15	80	96.4	17	2	US-08-743-894B-43	Sequence 43, Appl
16	79	95.2	16	2	US-08-743-894B-49	Sequence 49, Appl
17	79	95.2	17	2	US-08-743-894B-27	Sequence 27, Appl
18	79	95.2	17	2	US-08-743-894B-30	Sequence 30, Appl
19	79	95.2	17	2	US-08-743-894B-32	Sequence 32, Appl
20	78	95.2	17	2	US-08-743-894B-39	Sequence 39, Appl
21	78	94.0	17	2	US-08-743-894B-19	Sequence 19, Appl
22	78	94.0	17	2	US-08-743-894B-25	Sequence 25, Appl
23	78	94.0	17	2	US-08-743-894B-29	Sequence 29, Appl
24	78	94.0	17	2	US-08-743-894B-42	Sequence 42, Appl
25	78	94.0	17	2	US-08-743-894B-50	Sequence 50, Appl
26	77	92.8	17	2	US-08-743-894B-2	Sequence 2, Appli
27	77	92.8	17	2	US-08-743-894B-20	Sequence 20, Appl
28	77	92.8	17	2	US-08-743-894B-24	Sequence 24, Appl
29	77	92.8	17	2	US-08-743-894B-26	Sequence 26, Appl
30	77	92.8	17	2	US-08-743-894B-28	Sequence 28, Appl
31	77	92.8	17	2	US-08-743-894B-31	Sequence 31, Appl
32	77	92.8	17	2	US-08-743-894B-33	Sequence 33, Appl
33	77	92.8	17	2	US-08-743-894B-34	Sequence 34, Appl
34	77	92.8	17	2	US-08-743-894B-36	Sequence 36, Appl
35	77	92.8	17	2	US-08-743-894B-44	Sequence 44, Appl
36	77	92.8	17	2	US-08-743-894B-45	Sequence 45, Appl
37	77	92.8	17	2	US-08-743-894B-46	Sequence 46, Appl
38	77	92.8	24	4	US-09-962-360B-8	Sequence 8, Appl
39	77	92.8	116	4	US-09-962-360B-12	Sequence 12, Appl
40	75	90.4	17	2	US-08-743-894B-21	Sequence 21, Appl
41	75	90.4	17	2	US-08-743-894B-35	Sequence 35, Appl
42	75	90.4	17	2	US-08-743-894B-47	Sequence 47, Appl
43	74	89.2	17	2	US-08-743-894B-48	Sequence 48, Appl
44	74	89.2	15	2	US-08-743-894B-38	Sequence 38, Appl
45	74	89.2	17	2	US-08-743-894B-3	Sequence 3, Appli

ALIGNMENTS

```
RESULT 1
US-08-743-894B-1
; Sequence 1, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
;   APPLICANT: James J. Schmidt
;   APPLICANT: Karen A. Bostian
;   TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin E
;   NUMBER OF SEQUENCES: 56
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
;   STREET: USA MRMC - 504 Scott Street
;   CITY: FORT DETRICK
;   STATE: MARYLAND
;   COUNTRY: USA
;   ZIP: 21702-5012
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: Apple Macintosh
;   OPERATING SYSTEM: Macintosh 7.0
;   SOFTWARE: Microsoft Word 6.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/743,894B
;   FILING DATE: No. 5965699ember 6, 1996
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Charles H. Harris
;   REGISTRATION NUMBER: 34,616
;   REFERENCE/DOCKET NUMBER:
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (301) 619-2065
;   TELEFAX: (301) 619-7714
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 17 amino acids
;   TYPE: amino acid sequence
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
US-08-743-894B-1

Query Match             100.0%;  Score 83;  DB 2;  Length 17;
Best Local Similarity   100.0%;  Pred. No. 4.6e-08;
Matches   17;  Conservative  0;  Mismatches   0;  Indels  0;  Gaps  0;

Qy          1 SNKTRIDEANQRATKML 17
              |||||||||||||||||
Db          1 SNKTRIDEANQRATKML 17
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                 GenCore version 5.1.6
           Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    May 17, 2005, 15:34:49 ; Search time 134 seconds
                                    (without alignments)
                                    42.380 Million cell updates/sec

Title:          US-09-942-098-30
Perfect score:  83
Sequence:       1 SNKTRIDEANQRATKML 17

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters:      1432185

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published_Applications_AA:*
          1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
          2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
          3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
          4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
          5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
          6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
          7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
          8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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         10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
         11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
         12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
         13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
         14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
         15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
         16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
         17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
         18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
         19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
         20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	83	100.0	17	10	US-09-942-024-30	Sequence 30, Appl
2	83	100.0	17	10	US-09-942-098-30	Sequence 30, Appl
3	83	100.0	17	13	US-10-011-588-2	Sequence 2, Appli
4	83	100.0	17	15	US-10-261-161-52	Sequence 52, Appl
5	83	100.0	17	15	US-10-261-161-68	Sequence 68, Appl
6	83	100.0	18	10	US-09-942-024-32	Sequence 32, Appl
7	83	100.0	18	10	US-09-942-098-32	Sequence 32, Appl
8	83	100.0	18	15	US-10-261-161-54	Sequence 54, Appl
9	83	100.0	21	10	US-09-942-024-89	Sequence 89, Appl
10	83	100.0	21	10	US-09-942-098-89	Sequence 89, Appl
11	83	100.0	23	10	US-09-942-024-88	Sequence 88, Appl
12	83	100.0	23	10	US-09-942-098-88	Sequence 88, Appl
13	83	100.0	24	10	US-09-942-024-90	Sequence 90, Appl
14	83	100.0	24	10	US-09-942-098-90	Sequence 90, Appl
15	83	100.0	33	10	US-09-942-024-33	Sequence 33, Appl
16	83	100.0	33	10	US-09-942-024-37	Sequence 37, Appl
17	83	100.0	33	10	US-09-942-024-38	Sequence 38, Appl
18	83	100.0	33	10	US-09-942-098-33	Sequence 33, Appl
19	83	100.0	33	10	US-09-942-098-37	Sequence 37, Appl
20	83	100.0	33	10	US-09-942-098-38	Sequence 38, Appl
21	83	100.0	33	15	US-10-261-161-55	Sequence 55, Appl
22	83	100.0	33	15	US-10-261-161-59	Sequence 59, Appl
23	83	100.0	33	15	US-10-261-161-60	Sequence 60, Appl
24	83	100.0	116	10	US-09-962-360B-11	Sequence 11, Appl
25	83	100.0	203	10	US-09-942-024-14	Sequence 14, Appl
26	83	100.0	203	15	US-10-261-161-7	Sequence 7, Appli
27	83	100.0	206	10	US-09-942-024-2	Sequence 2, Appli
28	83	100.0	206	10	US-09-942-024-7	Sequence 7, Appli
29	83	100.0	206	10	US-09-942-024-12	Sequence 12, Appl
30	83	100.0	206	10	US-09-942-098-2	Sequence 2, Appli
31	83	100.0	206	10	US-09-942-098-7	Sequence 7, Appli
32	83	100.0	206	10	US-09-942-098-12	Sequence 12, Appl
33	83	100.0	206	15	US-10-261-161-4	Sequence 4, Appli
34	83	100.0	206	15	US-10-261-161-5	Sequence 5, Appli
35	83	100.0	206	15	US-10-261-161-109	Sequence 109, App
36	83	100.0	206	16	US-10-318-417-3	Sequence 3, Appli
37	83	96.4	17	10	US-09-942-024-55	Sequence 55, Appl
38	80	96.4	17	10	US-09-942-098-55	Sequence 55, Appl
39	80	96.4	17	15	US-10-261-161-80	Sequence 80, Appl
40	80	95.2	17	15	US-10-261-161-29	Sequence 29, Appl
41	79	95.2	16	10	US-09-942-024-29	Sequence 29, Appl
42	79	95.2	16	10	US-09-942-098-29	Sequence 29, Appl
43	79	95.2	16	15	US-10-261-161-51	Sequence 51, Appl
44	79	95.2	16	15	US-10-261-161-67	Sequence 67, Appl
45	79	95.2	17	10	US-09-942-024-31	Sequence 31, Appl

ALIGNMENTS

```
RESULT 1
US-09-942-024-30
; Sequence 30, Application US/09942024
; Publication No. US2003014365OA1
; GENERAL INFORMATION:
;   APPLICANT: Steward, Lance E.
;   APPLICANT: Fernandez-Salas, Ester
;   APPLICANT: Aoki, Kei Roger
;   TITLE OF INVENTION: Fret Protease Assays For Botulinum
;   TITLE OF INVENTION: Serotype A/E Toxins
;   FILE REFERENCE: P-AR 4803
;   CURRENT APPLICATION NUMBER: US/09/942,024
;   CURRENT FILING DATE: 2001-08-28
;   NUMBER OF SEQ ID NOS: 96
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-942-024-30

  Query Match             100.0%;  Score 83;  DB 10;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SNKTRIDEANQRATKML 17
              |||||||||||||||||
Db          1 SNKTRIDEANQRATKML 17

RESULT 2
US-09-942-098-30
; Sequence 30, Application US/09942098
; Publication No. US2003014365lA1
; GENERAL INFORMATION:
;   APPLICANT: Steward, Lance E.
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           GenCore version 5.1.6
        Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - protein search, using sw model

Run on:   May 17, 2005, 15:23:26 ; Search time 163 Seconds
                                    (without alignments)
                          40.337 Million cell updates/sec

Title:          US-09-942-098-30
Perfect score:  83
Sequence:       1 SNKTRIDEANQRATKML 17

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:  2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  A_Geneseq_16Dec04:*
         1: geneseqp1980s:*
         2: geneseqp1990s:*
         3: geneseqp2000s:*
         4: geneseqp2001s:*
         5: geneseqp2002s:*
         6: geneseqp2003as:*
         7: geneseqp2003bs:*
         8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	83	100.0	17	2	AAY44057	Aay44057 Human SNA
2	83	100.0	17	2	AAY44021	Aay44021 Amino aci
3	83	100.0	17	5	ABG69065	Abg69065 Human pol
4	83	100.0	17	6	AAE36675	Aae36675 Human SNA
5	83	100.0	17	7	ABW01731	Abw01731 Human SNA
6	83	100.0	17	8	ADM97046	Adm97046 Botulinum
7	83	100.0	17	8	ADM97062	Adm97062 Botulinum
8	83	100.0	18	6	AAE36677	Aae36677 Human SNA
9	83	100.0	18	7	ABW01733	Abw01733 Human SNA
10	83	100.0	18	8	ADM97048	Adm97048 Botulinum
11	83	100.0	19	4	AAB15586	Aab15586 Human SNA
12	83	100.0	19	8	ADP11171	Adp11171 SNAP 25 p
13	83	100.0	20	2	AAW30100	Aaw30100 Neurotran
14	83	100.0	20	7	ABW01798	Abw01798 FRET subs
15	83	100.0	21	6	AAE36734	Aae36734 Fret subs
16	83	100.0	21	7	ABW01790	Abw01790 FRET subs
17	83	100.0	23	6	AAE36733	Aae36733 Fret subs
18	83	100.0	23	7	ABW01789	Abw01789 FRET subs
19	83	100.0	24	6	AAE36735	Aae36735 FRET subs
20	83	100.0	24	7	ABW01791	Abw01791 FRET subs
21	83	100.0	26	2	AAW30099	Aaw30099 Neurotran
22	83	100.0	33	6	AAE36682	Aae36682 Goldfish
23	83	100.0	33	6	AAE36683	Aae36683 Goldfish
24	83	100.0	33	6	AAE36678	Aae36678 SNAP-25 p
25	83	100.0	33	7	ABW01739	Abw01739 Goldfish
26	83	100.0	33	7	ABW01734	Abw01734 Mouse SNA
27	83	100.0	33	7	ABW01738	Abw01738 Goldfish
28	83	100.0	33	8	ADM97054	Adm97054 Botulinum
29	83	100.0	33	8	ADM97053	Adm97053 Botulinum
30	83	100.0	33	8	ADM97049	Adm97049 Botulinum
31	83	100.0	37	2	AAW30097	Aaw30097 Neurotran
32	83	100.0	70	2	AAR86823	Aar86823 SNAP-25 r
33	83	100.0	86	4	AAB15584	Aab15584 Human SNA
34	83	100.0	86	4	ADP13169	Adp13169 SNAP 25 p
35	83	100.0	116	5	AAO15165	Aao15165 Clostridi
36	83	100.0	200	8	ADN11044	Adn11044 Murine SN
37	83	100.0	203	7	ABW01715	Abw01715 Goldfish
38	83	100.0	203	8	ADM97001	Adm97001 Goldfish
39	83	100.0	206	2	AAW30103	Aaw30103 Synaptoso
40	83	100.0	206	2	AAW43426	Aaw43426 Mouse syn
41	83	100.0	206	2	AAW79198	Aaw79198 Mouse SNA
42	83	100.0	206	4	AAU00246	Aau00246 Synaptoso
43	83	100.0	206	4	AAU00253	Aau00253 SNARE hom
44	83	100.0	206	4	AAU00252	Aau00252 SNARE hom
45	83	100.0	206	6	AAE36662	Aae36662 Human SNA

ALIGNMENTS

```
RESULT 1
AAY44057
ID   AAY44057 standard; peptide; 17 AA.
XX
AC   AAY44057;
XX
DT   18-JAN-2000  (first entry)
DE   Human SNAP25 (amino acids 187-203) analogue #36.
XX
KW   Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;
KW   fluorescamine; detection; human; synaptosomal protein; SNAP25;
KW   hydrolysis; amino group.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US5965699-A.
XX
PD   12-OCT-1999.
XX
PF   06-NOV-1996;      96US-00743894.
XX
PR   06-NOV-1996;      96US-00743894.
XX
PA   (USSA ) US SEC OF ARMY.
XX
PI   Bostian KA,   Schmidt JJ;
XX
DR   WPI; 1999-579939/49.
XX
PT   Quantitation of type A botulinum toxin.
XX
PS   Disclosure; Col 9; 28pp; English.
XX
CC   The invention relates to an enzymatic assay for the quantitation of type
CC   A botulinum toxin, by determining the proteolytic activity of botulinum
CC   neurotoxin type A using fluorescamine detection. Botulinum toxin A has
CC   been shown to cleave the synaptosomal neurotransmitter peptide SNAP25
CC   between residues 197-198. The method comprises adding an analogue (e.g.
CC   AAY44022-Y44076) of the SNAP25 peptide (AAY44021, amino acids 187-203 of
CC   human SNAP25) to a sample containing the botulinum toxin A so that
CC   hydrolysis of the peptide is initiated, then stopping hydrolysis of the
CC   peptide at different time points; and measuring the amount of hydrolysis
CC   at each time point by combining with a label capable of detecting free
CC   amino groups resulting from the hydrolysis. The amount of botulinum toxin
CC   A present in the sample is determined by comparing measurements with the
CC   amount of label produced from a known concentration of toxin measured
```